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AMENDMENT TO THE CLAIMS

Please cancel claims 7, 10-12, 30-42, 57-66, 71, and 73-75 without prejudice to pursue these claims in a continuation application, amend claims 1-3, 5, 6, 8, 13-29, 43-45, and 67-70, 72, and 76-81, and insert new claims 82-85, as follows.

1. (Currently Amended) A computer implemented method for classifying chromatograms determining a similarity or dissimilarity between chromatogram data sets, comprising:
 - a) receiving a first chromatogram data corresponding to a first chromatogram;
 - b) adjusting the first chromatogram data in a first region of interest by centering an analysis window around one or more trace features in the first region of interest;
 - c) reducing the first chromatogram data to a first data set, based at least on an average time for the chromatogram data in the first region of interest by determining an integral of the first chromatogram data and plotting against a time axis, determining a set of time points, and forming arrays of first data set values based upon the set of time points and corresponding integral values for the set of time points;

receiving a second chromatogram data corresponding to a second chromatogram;

adjusting the second chromatogram data in a second region of interest by centering an analysis window around one or more trace features in the second region of interest;

reducing the second chromatogram data to a second data set based at least on an average time for the chromatogram data in the second region of interest by determining an integral of the second chromatogram data and plotting against a time axis, determining a set of time points, and forming arrays of first data set values based upon the set of time points and corresponding integral values for the set of time points;

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- d) repeating the steps of (a) to (c) for at least one additional chromatogram data;
- e) choosing a reference data set from among the data sets obtained from the steps of (a) to (d); and
- f) comparing the first data set and the second data set to produce a comparison result the reference data set to a remaining data set not chosen in step (e) to determine a similarity or dissimilarity between the reference data set and the remaining data set; and
- classifying the first and second chromatograms based on the comparison result.
2. (Currently Amended) The method of claim 1, ~~in which, wherein~~ the acts of adjusting the first and second chromatogram data ~~comprise~~ comprises performing baseline correction.
3. (Currently Amended) The method of claim 1, further comprising:
- identifying the first region of interest in the first chromatogram data before adjusting the first chromatogram data; and
- identifying the second region of interest in the second chromatogram data before adjusting the second chromatogram data.
4. (Canceled)
5. (Currently Amended) The method of claim 1, ~~in which, wherein~~ the act of centering comprises:
- determining an average time for the given region of interest; and
- centering the analysis window around the average time.

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6. (Currently Amended) The method of claim 1, further comprising:

~~filtering the first and second chromatogram data to identify establishing a threshold value for a peak characteristic selected from the group consisting of peak height, peak shape, peak position, peak slope, and peak size; and~~

~~determining whether a value associated with the chromatogram data exceeds the threshold value, wherein the value exceeding the threshold value indicates the chromatogram data as flawed bad data.~~

7. (Canceled)

8. (Currently Amended) The method of claim 1 in which, ~~wherein the acts of reducing the first and second chromatogram data to the first and second data sets comprise~~ ~~comprises~~ determining arrays ~~an array of data set values directly from the first and second~~ ~~from the chromatogram data.~~

9-12. (Canceled)

13. (Currently Amended) The method of claim 12, further comprising:

~~mapping results a result of the comparing the reference chromatogram against one or both of the first and second chromatogram data.~~

14. (Currently Amended) The method of claim 13 in which, ~~wherein the mapping is performed to produce a two-dimensional cluster map.~~

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15. (Currently Amended) The method of claim 1-in which, wherein the act of comparing comprises determining a degree of similarity between the first and second data sets reference data set and the remaining data set.

16. (Currently Amended) The method of claim 1-in which, wherein the act of comparing comprises determining a degree of dissimilarity between the first and second data sets reference data set and the remaining data set.

17. (Currently Amended) The method of claim 1-in which, wherein the act of comparing comprises determining distance between vectors associated with the first and second data sets reference data set and the remaining data set.

18. (Currently Amended) The method of claim 1-in which, wherein the first and second chromatogram data relate relates to DNA analysis, wherein and the reduced chromatogram data excludes a main DNA peak and fully encapsulate encapsulates a possible sequence variation peak.

19. (Currently Amended) A system for classifying comparing chromatograms, comprising:
a data storage device to store chromatogram data;
a communications interface adaptable to receive chromatogram data from the data storage device;
a data adjustment module to adjust the chromatogram data;
a reduction module to reduce the chromatogram data to a data set based at least on an

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average time for the chromatogram data in a region of interest; and
a comparison module to compare the reduced data set against other chromatogram data sets;
and
~~a classification module to classify the chromatogram corresponding to the reduced data set.~~

20. (Currently Amended) The system of claim 19, further comprising a data filter.
21. (Currently Amended) The system of claim 20 ~~in which, wherein~~ the data filter performs filtering based upon criteria selected from the group consisting of peak height, peak area, peak shape, peak position, peak slope, and peak size.
22. (Currently Amended) The system of claim 19 ~~in which, wherein~~ the data adjustment module performs baseline correction for the chromatogram data in a region of interest.
23. (Currently Amended) The system of claim 19 ~~in which, wherein~~ the data adjustment module centers the analysis window around one or more trace features in a region of interest.
24. (Currently Amended) The system of claim 19 ~~in which, wherein~~ the reduction module determines an array of data set values ~~directly~~ from the chromatogram data.
25. (Currently Amended) The system of claim 24 ~~in which the array of data set values are formed, wherein the reduction module is configured to determine the array of data set values by:~~
selecting a set of time points in the first and second chromatogram data;

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determining amplitude values corresponding to the set of time points; and
forming the arrays of data set values based upon the set of time points and their
corresponding amplitude values.

26. (Currently Amended) The system of claim 19, ~~in which, wherein~~ the reduction module determines an array of data set values ~~based upon by~~:
determining an integral of the chromatogram data and plotting against a time axis;
determining a set of time points;
forming the arrays of data set values based upon the set of time points and corresponding integral values for the set of time points.
27. (Currently Amended) The system of claim 19, wherein the data adjustment module, the reduction module, or the comparison module is implemented using one or more programmable logic devices.
28. (Currently Amended) The system of claim 19, further comprising a mapping module to map results from the comparison module.
29. (Currently Amended) The system of claim 28, further comprising a user interface to display results from the comparison module.
- 30-42. (Canceled)

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43. (Currently Amended) A computer usable medium having stored thereon a sequence of instructions which, when executed by a processor, causes the processor to execute a process for classifying chromatograms, said process comprising:

- a) receiving a ~~first~~ chromatogram data corresponding to a ~~first~~ chromatogram;
- b) adjusting the ~~first~~ chromatogram data in a ~~first~~ region of interest by centering an analysis window around one or more trace features in the ~~first~~ region of interest;
- c) reducing the ~~first~~ chromatogram data to a ~~first~~ data set, based at least on an average time for the chromatogram data in the ~~first~~ region of interest by determining an integral of the ~~first~~ chromatogram data and plotting against a time axis, determining a set of time points, and forming arrays of ~~first~~ data set values based upon the set of time points and corresponding integral values for the set of time points;
- receiving a ~~second~~ chromatogram data corresponding to a ~~second~~ chromatogram;
- adjusting the ~~second~~ chromatogram data in a ~~second~~ region of interest by centering an analysis window around one or more trace features in the ~~second~~ region of interest;
- reducing the ~~second~~ chromatogram data to a ~~second~~ data set, based at least on an average time for the chromatogram data in the ~~second~~ region of interest by determining an integral of the ~~second~~ chromatogram data and plotting against a time axis, determining a set of time points, and forming arrays of ~~second~~ data set values based upon the set of time points and corresponding integral values for the set of time points;
- d) repeating the steps of (a) to (c) for at least one time;
- e) choosing a reference data set from among the data set obtained from steps (a) to (d); and

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f) comparing the first data set and the second data set to produce a comparison result the reference data set to a remaining data set not chosen in step (e) to determine a similarity or dissimilarity between the reference data set and the remaining data set; and classifying the first and second chromatograms based on the comparison result.

44. (Currently Amended) The method of claim 1, further comprising determining the average time for chromatogram data in the first region of interest, and determining the average time for chromatogram data in the second region of interest.

45. (Currently Amended) The method of claim 44, wherein the determining the average time for chromatogram data in the ~~first and second regions~~ region of interest is performed based on

$$\bar{t} = \left(\sum_{i=0}^{i=n} y_i^2 * t_i \right) / \sum_{i=0}^{i=n} y_i^2 .$$

46-66. (Canceled)

67. (Currently Amended) The medium of claim 43 ~~in which~~, wherein the adjusting the first and second chromatogram data comprise ~~comprises~~ performing baseline correction.

68. (Currently Amended) The medium of claim 43, wherein the process further comprises:
identifying the first region of interest in the first chromatogram data before adjusting the first chromatogram data; and
identifying the second region of interest in the second chromatogram data before adjusting

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~~the second chromatogram data.~~

69. (Currently Amended) The medium of claim 43 ~~in which, wherein the~~ centering comprises:
determining an average time for the ~~given~~ region of interest; and
centering the analysis window around the average time.

70. (Currently Amended) The medium of claim 43 wherein the process further comprises:
~~filtering the first and second chromatogram data to identify establishing a threshold value for a peak characteristic selected from the group consisting of peak height, peak shape, peak position, peak slope, and peak size; and~~
~~determining whether a value associated with the chromatogram data exceeds the threshold value, wherein the value exceeding the threshold value indicates the chromatogram data as flawed bad data.~~

71. (Canceled)

72. (Currently Amended) The medium of claim 43 ~~in which, wherein the~~ reducing the first and second chromatogram data to the first and second data sets comprise ~~comprises~~ determining arrays ~~an array of data set values directly from the first and second from the chromatogram data.~~

73-75. (Canceled)

76. (Currently Amended) The medium of claim 75, wherein the process further comprises:

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~~mapping results a result of the comparing the reference chromatogram against one or both of the first and second chromatogram data.~~

77. (Currently Amended) The medium of claim 76 ~~in which, wherein the comparing is performed to produce~~ a two-dimensional cluster map.

78. (Currently Amended) The medium of claim 43 ~~in which, wherein the comparing comprises determining a degree of similarity between the first and second data sets reference data set and the remaining data set.~~

79. (Currently Amended) The medium of claim 43 ~~in which, wherein the comparing comprises determining a degree of dissimilarity between the first and second data sets reference data set and the remaining data set.~~

80. (Currently Amended) The medium of claim 43 ~~in which, wherein the comparing comprises determining distance between vectors associated with the first and second data sets reference data set and the remaining data set.~~

81. (Currently Amended) The medium of claim 43 ~~in which, wherein the first and second chromatogram data relate relates to DNA analysis, wherein and the reduced chromatogram data excludes a main DNA peak and fully encapsulate encapsulates a possible sequence variation peak.~~

82. (New) The method of claim 1, further comprising determining a presence of a sequence

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variation based on the comparing.

83. (New) The method of claim 1, wherein the chromatogram data comprises DHPLC chromatogram data.

84. (New) A computer implemented method for determining a similarity or dissimilarity between chromatogram data sets, comprising:

- a) receiving a chromatogram data;
- b) adjusting the chromatogram data in a region of interest by centering an analysis window around one or more trace features in the region of interest;
- c) reducing the chromatogram data to a data set based upon a consistent positioning across chromatograms;
- d) repeating the steps of (a) to (c) for at least one additional chromatogram data;
- e) choosing a reference data set from among the data sets obtained from the steps of (a) to (d); and
- f) comparing the reference data set to a remaining data set not chosen in step (e) to determine a similarity or dissimilarity between the reference data set and the remaining data set.

85. (New) A computer implemented method for determining a similarity or dissimilarity between chromatogram data sets, comprising:

- a) receiving a chromatogram data;
- b) adjusting the chromatogram data in a region of interest by centering an analysis window around one or more trace features in the region of interest;

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- c) reducing the chromatogram data to a data set based on an average time for the chromatogram data in the region of interest;
- d) repeating the steps of (a) to (c) for at least one additional chromatogram data;
- e) choosing a reference data set from among the data sets obtained from the steps of (a) to (d); and
- f) comparing the reference data set to a remaining data set not chosen in step (e) to determine a similarity or dissimilarity between the reference data set and the remaining data set.